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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 15:04:29 ; Search time 15.0398 Seconds
(without alignment)

2160.495 Million cell updates/sec

Title: US-09-807-933B-7

Perfect score: 1826

Sequence: 1 MKFTVATISVALALSSA.....TFKEVTPALVTRSGCERK 338

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	758.5	41.5	229	2 UC7308	cellulase (EC 3.2.
2	568.5	31.7	511	2 S10527	endoglucanase B pr
3	525.5	28.8	393	2 S59499	cellulase eg11 - s
4	233.5	12.8	471	1 A26160	cellulose 1,4-beta
5	233.5	12.8	471	1 A38979	cellulose 1,4-beta
6	198.5	10.9	418	1 S28372	cellulase (EC 3.2.
7	198	10.8	410	1 S68153	cellulase (EC 3.2.
8	181	9.9	438	1 S70602	cellulose 1,4-beta
9	174.5	9.6	533	2 T33912	hypothetical prote
10	169.5	9.3	475	2 S49886	probable membrane
11	159.5	8.7	4776	2 E95206	cell wall surface
12	159	8.7	2395	1 S50820	surface protein ty
13	156	8.5	605	2 T33913	hypothetical prote
14	155	8.5	1428	2 T08852	lubricin A - Callif
15	153	8.4	503	2 S63257	probable membrane
16	150	8.2	662	2 A45155	mucin FIM-C.1 - Af
17	148.5	8.1	797	1 VGBEX1	glycoprotein X pre
18	148.5	8.1	1275	2 T33369	hypothetical prote
19	148	8.1	402	2 E86185	hypothetical prote
20	147.5	8.1	463	2 T38444	hypothetical prote
21	147.5	8.1	867	2 T45463	membrane glycoprot
22	147	8.1	542	2 S64030	probable membrane
23	147	8.1	937	2 S58135	hypothetically regul
24	147	8.1	1777	2 T34369	hypothetical prote
25	146.5	8.0	1032	2 T34433	hypothetical prote
26	146.5	8.0	2232	2 T34434	microfilament shea
27	146	8.0	354	2 T46740	carboxymethylcellu
28	143	7.8	962	2 S03818	mucin-like glycopr
29	143	7.8	1832	2 T31113	

30	142	7.8	263	2 S01360	salivary glue prot
31	142	7.8	417	2 UC7092	Paul protein - fis
32	141.5	7.7	888	2 T46726	secreted acid phos
33	141	7.7	556	2 S51892	probable membrane
34	140.5	7.7	329	2 S38082	pathogenesis-relat
35	140	7.7	537	2 B33485	spore coat protein
36	139.5	7.6	720	1 A55160	trig protein - fruit
37	139	7.6	242	2 S60143	cellulase (EC 3.2.
38	139	7.6	304	2 T15922	hypothetical prote
39	139	7.6	344	2 T40167	hypothetical prote
40	139	7.6	748	2 S19652	celluloxetrinase C
41	139	7.6	786	1 A47547	serine proteinase
42	138.5	7.6	378	2 S61992	Sigl1 protein - yea
43	138.5	7.6	388	1 JC5461	cellulase (EC 3.2.
44	138.5	7.6	2639	2 T31328	fibroin - Chinese
45	138	7.6	513	1 EUTQI	cellulose 1,4-beta

ALIGNMENTS

RESULT 1
UC7308
cellulase (EC 3.2.1.4) - Scopulariopsis brevicaulis
N:Alternate names: endoglucanase I
C:Species: Scopulariopsis brevicaulis
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: UC7308, PC7087
R:Nakatsui, F.; Kawaguchi, T.; Takada, G.; Sumitani, J.; Moriyama, Y.; Arai, M.
Biosci. Biotechnol. Biochem. 64, 1238-1246, 2000
A>Title: Cloning and sequencing of an endoglucanase gene from Scopulariopsis brevicaulis
A:Reference number: JC7308
A:Accession: UC7308
A:Molecule type: DNA
A:Residues: 1-229 <NAK>
A:Experimental source: strain TOF-1212
A:Accession: PC7087
A:Molecule type: protein
A:Residues: 21-37,149-164 <NA2>
C:Genetics:
A:Gene: eg1
A:introns: 147/3
C:Keywords: glycosidase; hydrolase

Query Match 41.5%; Score 758.5; DB 2; Length 229;
Best Local Similarity 62.8%; Pred. No. 6.3e-42;
Matches 130; Conservative 30; Mismatches 44; Indels 3; Gaps 3;

QY	134	SGSGSTRYMDCKASGSPGKASVT-GPVDTCASNGISLIDAN-AQSGCN-GGNGFMCN	190
DB	22	SGGTTRRYMDCCPKSPGKAPLSGCPMTCDINDPLDDGLTBSGCPGGAYVCS	81
QY	191	NNQPAVNDLAYPAAASINAGNCCGCEYLTFTSGAAGSKRVVQVNTGGDGS	250
DB	82	SHSPWAVNDLAYGMAAVNIGQTESDWCACYELEFTGAVSGKMIVQATNTGGDIGN	141
QY	251	NHPLQWPGGSGVGFNGCAQWGA.PNDGKGRVGVSSVSQCAILPSALQGGKRRPWF	310
DB	142	NHPIAPMGSGVGIFNGCTDQWSPNMGWRVGVVHTRADCDSPKALKAGCEWRPWF	201
QY	311	KNSDNPMTFKKVCPCPAELVTRSGCER 337	
DB	202	GGTNDPVSFRFVECPALVOKSQQR 228	

RESULT 2
S10527
endoglucanase B precursor - Pseudomonas fluorescens
C:Species: Pseudomonas fluorescens
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Oct-1999
C:Accession: S10527
R:Gilbert, H.J.; Hall, J.; Hazlewood, G.P.; Ferreira, L.M.A.
Mol. Microbiol. 4, 759-767, 1990

DB 86 MCF--DDETDPTLAFGFA--FTTGESDTCACFYAFEHF--AQGAMKKNKLIQVT 14

C;Superfamily: cellulose 1,4-beta-cellobiosidase II; fungal cellulose-binding domain homolog
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

ding domain not

A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: R95206
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4776 <CUR>
A:Cross-references: GB:AE005672; PIDN:AAK75846.1; PID:G14973269; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI772

Query Match 8.7%; Score 159.5; DB 2; Length 4776;
Best Local Similarity 25.2%; Pred. No. 0.026;
Matches 71; Conservative 36; Mismatches 118; Indels 57; Gaps 8;

6 AITSIATVALSSAEASCSVYGGCGIGMSGPTCEGSGPTCAEGNKYVQCLPGS 65
4527 ASTSASVSASTSASASTSASASTSASASTSASASTSASASTSASASTSASASTS 4586
66 HSNNAAG-NASTTKTSTKTSTTTAKATATVTTKTTTCTTTAAASTSTSSA 124
4587 ASASASISASBASASTSASASTS-ASASASTSASASTSASASTSASASTSASA 4645
125 GYKVISGKSGSGSTTRYWDCCKASCNMPKASVTGPVDTCASNGISILDANAQSGCNG 184
4646 S---ASTSASASTS---ASASASTSASASTSASASTSAS---ASASTSAS-- 4692
185 NGPFCNNQPMVAUNDELAYGPAASIASGNSAGCCGCTELTFTSGAASGKMYVQVNT 244
4693 -----ASASTSASASTSASASTSASASTSVNSNHSNS--QVQNT 4729

245 GGDLSNHFPLQMPGGVGFNCGCAQWGAIPNDMGARYGV 286
4730 SGSTGKSQKEL-----PNTGTSSISGV 4752

RESULT 12
550820
Surface protein type 51B - Parametium tetraurelia
C:Species: Parametium tetraurelia
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 07-Dec-1999
C:Accession: S50820
R:Scott, J.; Leech, C.; Forney, J.
Nucleic Acids Res. 22, 5079-5084, 1994
A:Title: Analysis of the micronuclear B type surface protein gene in Parametium tetraurelia
A:Reference number: S50820; MUID:9509630; PMID:7800503
A:Accession: S50820
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-2395 <SCO>
A:Cross-references: EMBL:U07603; NID:G467226; PIDN:AA81947.1; PID:G467227
C:Genetics:
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994
A:Genetic code: SGC5
A:introns: 472/3; 1310/3; 1821/3
C:Superfamily: G surface protein

Query Match 8.7%; Score 159; DB 1; Length 2395;
Best Local Similarity 23.3%; Pred. No. 0.015;
Matches 89; Conservative 37; Mismatches 152; Indels 104; Gaps 21;

16 LSSSABAAAGCSVYGGCGIGMSGPTCE-----SGSTCV---AQEGNK----- 56
1948 VNSDGSKACPR-YTCKSLMNSDPTCKMISNOCTTNGSNCIG:ITLCESTNIDGGCVSG 2006
57 YYSOCLPESHNNAGNASTTKTSTTTAKATATVTTKTTTCTTTAAASTSTSSA 116
2007 YDGAACI---QSVPLMNSDPRVCKRYTSC---ADAFYTHSDCQTASKCTTNGTTCI 2059
117 STSTSS-----AGKVISGKSGSGSTTRYWDCCKASGMPKASVTG----- 160
2060 ALGACSSYTTGACGYFNDKGLALTSALTSTGICL--WDTTASGCRDSCADLTGTTHAT 2117
161 ---PVDTCASNGISILDANA-----QSGCN---GSGNFMG-----NNNQPMVA----- 196

2118 CSSQLSTCTSDGTSCLVAGACTSYTQFACCTAVAGSDG-ICVYELASTNNNTAKCRLLA 2176
197 ---VNDELAYGPAASIASGNSAGMCWCC---GCEYL---FTSGAASGKMYVQVNTG 245
2177 CADIQNSTNVCVVALSSCVSNAGTACIACANCTYTTKTACNSGGIDGICVFTQSTATG 2236
246 GDLGSNHFPLQMPGGVGFNCGC-----AAQMGAPNDMGARYG-GVSSV-SDCA-- 293
2237 AAGT-----GTCLMTACTTANSDDVACQAAADRCSTWTAASGTGTTAVASKCATH 2287
294 --SLPSALQAGCKWRFNWPKN 313
2288 TCATNQATNGACTRFILNMDKKT 2309

RESULT 13
733913
hypotheical protein Y25C1A.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T33913
R:Kalicki, J.; Smith, A.; Gibson, A.
submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid Y25C1A.
A:Reference number: Z21437
A:Accession: T33913
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-605 <KAL>
A:Cross-references: EMBL:AF125459; PIDN:AAD12833.1; GSPDB:GN00020; CESP:Y25C1A.3
A:Experimental source: strain Bristol N2; clone Y25C1A
C:Genetics:
A:Gene: CESP:Y25C1A.3
A:Map position: 2
A:introns: 392/3; 429/1; 567/3

Query Match 8.5%; Score 156; DB 2; Length 605;
Best Local Similarity 21.7%; Pred. No. 0.0067;
Matches 93; Conservative 37; Mismatches 183; Indels 116; Gaps 14;

4 TVALTSIAVALALSSAEASCSVYGGCGIGMSGPTCEGSGPTCAEQNKYVQCLP 63
190 TAAAGSTATTAAAGSTATTAAAGSTATTAA--GGSTATTAAAGSTATTAAAGSTATTAA 247
64 GS-HSNNAAGNASTTKTSTTTAKATATVTTKTTTCTTTAAASTSTSS 122
248 GSTASTAAGSTATTAAAGSTATTAAAGSTATTAAAGSTATTAAAGSTATTAAAGSTAST 307
123 SAGKVISGKSGSGSTTRYWDC-----CKASCNMPKASVTGPVDTCASNGISILD 174
308 AAGGSTATTAAAGSTATTAAAGSTATTAAAGSTATTAAAGSTATTAAAGSTATTAAAGST 367
175 ANA-QSGCNGGNGFMGCNNQPMVAUNDELAYGFNA----- 207
368 SPAPAAACEPEYKRFNRPSPGWCIKVFTGY-FAAQIDABRCAQAGALITGLQNDALY 426
208 -----ASIASGNSAGCCGCTELTFTSGAASGKMYV---Q 240
427 IQSSLISQIKOPASVWIGIKRKASCVGKPDACCTTQSPFEWTDSDAGVNGVFKQO 486
241 VTNNGDL-----GSNHFPLQMPGGVGFNCGCAQMGAPNDMGARY 283
487 PDNGKALNDDCALLASRPTTIAAGTYTAQMED-----VNCIAFTFAANA--ARKT 538
284 GGVSSVSDCASLPALQAGCKWRFNWPKNSDNPT-----MTEKEVTCPEAL 329
539 GGYA-----CGGQPTTCQPG--WKF-----FDRPTGCMKVFYTGPHYQADABKACQAVG 587
330 TTRSGCERK 338
588 ATLSIOHK 596

RESULT 14

T08852
 Iustirin A - California red abalone
 C:Species: Halictia rufescens (California red abalone)
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C/Accession: T08852
 R:Shen, X.; Belcher, A.M.; Hanama, P.K.; Stucky, G.D.; Morse, D.E.
 J. Biol. Chem. 272, 32472-32481, 1997
 A>Title: Molecular cloning and characterization of Iustirin A, a matrix protein from shell
 A/Reference number: Z16496; PMID:9405458
 A/Accession: T08852
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1428 <SHE>
 A/Cross-references: EMBL:AF023459; NID:g2723361; PION:AB95154.1; PID:g2723362
 A:Experimental source: tissue type mantle (shell and pearl nacre); cell type pallial
 C:Superfamily: antileukoprotease repeat homology
 C:Keywords: extracellular matrix; extracellular protein
 F:1382-1426/Domain: antileukoprotease repeat homology <ALP>

Query Match 8.5%; Score 155; DB 2; Length 1428;

Best Local Similarity 23.1%; Pred. No. 0.017;
 Matches 66; Conservative 51; Mismatches 117; Indels 52; Gaps 9;

DB 17 SSSAFAASCSVYGCQCGIGMSGPTCCSGSTCVAGQENKTYQCCLPGSHNNAGNASGT 76
 986 SSSGSGSSSSSSSGSTGSG-----SGSGSGSSSSSGSGSSSASGSSGSSSSSS 1037
 QY 77 KKTSTKTSTTAKATATVTTKTVTKTSTTTTAAASTSTSSAGYKVIISGKSGS 136
 DB 1038 SSSSSSGSSSGSGSSSSSASGSSSGSSSGSSSGSSSAG-----SGSSSGS 1092
 QY 137 GSTTRWPCCKASCMPKASVTPGVDTCASNGISILDANAQSCNGNGFMGNNOPIWA 196
 DB 1093 GSGS-----SSGSGSGSGSGSSSGSSSGSSSVSNMTGSSSGSG--SGSSSWS 1144
 QY 197 VNDELAYFPAASSTAGSNAGCCGCELTFTSGAAGKRVVQVNTGDLGSNHFIDQ 256
 DB 1145 -----GSGSSSGTSGSSSW-----FGSGSSG-----SGDSSSG-----S 1176
 QY 257 MPGGVGIVFNGCAQWGAQPNQMGARYGVSSVSDCASLPSALQAG 302
 DB 1177 SSSAFAASCSVYGCQCGIGMSGPTCCSGSTCVAGQENKTYQCCLPGSHNNAGNASGT 1219

RESULT 15

S63257
 Probable membrane protein YNL283c - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein N0583

C/Species: Saccharomyces cerevisiae

C/Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 06-Feb-1998

C/Accession: S63257

R:Messenguy, F.; Dubois, E.; Vierendeels, F.; Scherens, B.; Pierard, A.; Glandsdorff, N.
 submitted to the Protein Sequence Database, April 1996

A/Reference number: S63245

A/Accession: S63257

A/Molecule type: DNA

A/Residues: 1-503 <MES>

A/Cross-references: EMBL:Z71559; NID:g1302356; PID:e239724; PID:g1302357; MIPS:YNL283c

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:WSC2

A/Cross-references: SGD:S0005227; MIPS:YNL283c

A/Map position: 14L

C/Keywords: transmembrane protein

F:330-346/Domain: transmembrane #status predicted <TMM>

Query Match 8.4%; Score 153; DB 2; Length 503;
 Best Local Similarity 20.7%; Pred. No. 0.0089;
 Matches 73; Conservative 50; Mismatches 115; Indels 114; Gaps 11;
 QY 17 SSSAFAASCSVYGCQCGIGMSGPTCCSGSTCVAGQENK 56

DB 91 SSKCDVSCAGMPYQNCGGSSAMNVYINNAASTADSTSTASTSTSSSTSVSKSTK 150
 QY 57 YYSQCLPGSHNNAGNASSTKSTSTSTT-----AKATATVTTKVTKTSTKT-- 106
 DB 151 LDTSTSTSSATATSSSSSTSTSTSTSTSSSSSSSSSTSTSTSTSTSTSTSTSS 210
 QY 107 ---TTKTSTTAAAS-----TSTSSAGYKVIISGKSGS--GSTTRWPC-- 146
 DB 211 SPSTSTSSSTSSSST 270
 QY 147 -----KSCSWPKASVTPGVDTCASNGISILDANAQSCNGNGFMGNNOPIWA 187
 DB 271 QSVVSOANQASTTFTRTSVATVSTSSSTSSSLNGKSSSSKSLGGAIAAGVAVG 330
 QY 188 WC-----NNQPMVNDLAYGFAAASAGSNEAG 217
 DB 331 VCGTVALALALFFPVMKKRRQSSQVLDLETKQYQPSLGADADNPVIPPASSTN--- 387
 QY 218 WCCGCELTFTSGAASGKRVVQVNTGDLGSNHFIDQMPGGVGIVFNGCA 269
 DB 388 -----WHIPSRNNTALSK-----NTASTPATYDLPAPAGGRDSITGDA 427

Search completed: June 18, 2003, 17:16:18
 Job time : 16.0398 sec